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TECH CENTER 1600/2900

- 1 -

SEQUENCE LISTING

<110> KLIEWER, Stacey A.
JONES, Stacey A.
WILLSON, Timothy M.

<120> AN ORPHAN NUCLEAR RECEPTOR

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<140> 09/276,935

<141> 1999-03-26

<150> 60/079,593

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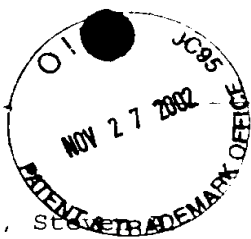
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35 40 45
Ser His Phe Lys Asn Phe Arg Leu Pro Gly Val Leu Ser Ser Gly Cys
50 55 60
Glu Leu Pro Glu Ser Leu Gln Ala Pro Ser Arg Glu Glu Ala Ala Lys
65 70 75 80
Trp Ser Gln Val Arg Lys Asp Leu Cys Ser Leu Lys Val Ser Leu Gln
85 90 95
Leu Arg Gly Glu Asp Gly Ser Val Trp Asn Tyr Lys Pro Pro Ala Asp
100 105 110
Ser Gly Gly Lys Glu Ile Phe Ser Leu Leu Pro His Met Ala Asp Met
115 120 125

Full
DI
cont

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Ala	Ala	Phe	Glu	Leu	Cys	Gln	Leu	Arg	Phe	Asn	Thr	Val	Phe	Asn	Ala
				165						170				175	
Glu	Thr	Gly	Thr	Trp	Glu	Cys	Gly	Arg	Leu	Ser	Tyr	Cys	Leu	Glu	Asp
		180						185					190		
Thr	Ala	Gly	Gly	Phe	Gln	Gln	Leu	Leu	Leu	Glu	Pro	Met	Leu	Lys	Phe
		195					200					205			
His	Tyr	Met	Leu	Lys	Lys	Leu	Gln	Leu	His	Glu	Glu	Glu	Tyr	Val	Leu
		210				215						220			
Met	Gln	Ala	Ile	Ser	Leu	Phe	Ser	Pro	Asp	Arg	Pro	Gly	Val	Leu	Gln
225					230					235				240	
His	Arg	Val	Val	Asp	Gln	Leu	Gln	Glu	Gln	Phe	Ala	Ile	Thr	Leu	Lys
				245						250				255	
Ser	Tyr	Ile	Glu	Cys	Asn	Arg	Pro	Gln	Pro	Ala	His	Arg	Phe	Leu	Phe
			260					265					270		
Leu	Lys	Ile	Met	Ala	Met	Leu	Thr	Glu	Leu	Arg	Ser	Ile	Asn	Ala	Gln
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His	Thr	Gln	Arg	Leu	Leu	Arg	Ile	Gln	Asp	Ile	His	Pro	Phe	Ala	Thr
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			20					25					30		
Asn	Met	Gly	Leu	Asn	Pro	Ser	Ser	Pro	Asn	Asp	Pro	Val	Thr	Asn	Ile
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Cys	Gln	Ala	Ala	Asp	Lys	Gln	Leu	Phe	Thr	Leu	Val	Glu	Trp	Ala	Lys
	50					55					60				
Arg	Ile	Pro	His	Phe	Ser	Glu	Leu	Pro	Leu	Asp	Asp	Gln	Val	Ile	Leu
65					70					75				80	
Leu	Arg	Ala	Gly	Trp	Asn	Glu	Leu	Leu	Ile	Ala	Ser	Phe	Ser	His	Arg
				85					90					95	
Ser	Ile	Ala	Val	Lys	Asp	Gly	Ile	Leu	Leu	Ala	Thr	Gly	Leu	His	Val
			100					105					110		
His	Arg	Asn	Ser	Ala	His	Ser	Ala	Gly	Val	Gly	Ala	Ile	Phe	Asp	Arg
		115					120					125			
Val	Leu	Thr	Glu	Leu	Val	Ser	Lys	Met	Arg	Asp	Met	Gln	Met	Asp	Lys
		130					135					140			

Thr	Glu	Leu	Gly	Cys	Leu	Arg	Ala	Ile	Val	Leu	Phe	Asn	Pro	Asp	Ser
145					150					155					160
Lys	Gly	Leu	Ser	Asn	Pro	Ala	Glu	Val	Glu	Ala	Leu	Arg	Glu	Lys	Val
				165					170					175	
Tyr	Ala	Ser	Leu	Glu	Ala	Tyr	Cys	Lys	His	Lys	Tyr	Pro	Glu	Gln	Pro
			180					185					190		
Gly	Arg	Phe	Ala	Lys	Leu	Leu	Leu	Arg	Leu	Pro	Ala	Leu	Arg	Ser	Ile
		195					200				205				
Gly	Leu	Lys	Cys	Leu	Glu	His	Leu	Phe	Phe	Phe	Lys	Leu	Ile	Gly	Asp
	210					215					220				
Thr	Pro	Ile	Asp	Thr	Phe	Leu	Met	Glu	Met	Leu	Glu	Ala	Pro	His	Gln
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Met	Thr														

<210> 13

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<212> DNA

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cggtcctctg	gtaaagctac	tccttgatcg	atcctttgca	ccggattgtt	caaagtggac	240
cccaggggag	aagtcggagc	aaagaactta	ccaccaagca	gtccaagagg	cccagaagca	300
aacctggagg	tgagacccaa	agaaagctgg	aaccatgctg	actttgtaca	ctgtgaggac	360
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ggatgcaagg	gctttttcag	gagggccatg	aaacgcaacg	cccggctgag	gtgccccttc	540
cggaagggcg	cctgcgagat	cacccggaag	acccggcgac	agtgccaggc	ctgccgcctg	600
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Sub
D1
Cont

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tcagtctgta gggagtgaag ccacagactc ttacgtggag agtgactga cctgtaggtc 1860
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aatccctcag atcccactaa agtgtcaagg tgtggaagg accaagcgac caaggatagg 1980
ccatctgggg tctatgccca catacccacg tttgttcgct tcttgagtct tttcattgct 2040
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<213> Artificial Sequence

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      20           25           30
Glu Glu Val Gly Gly Pro Gln Ile Cys Arg Val Cys Gly Asp Lys Ala
      35           40           45
Thr Gly Tyr His Phe Asn Val Met Thr Cys Glu Gly Cys Lys Gly Phe
      50           55           60
Phe Arg Arg Ala Met Lys Arg Asn Ala Arg Leu Arg Cys Pro Phe Arg
      65           70           75           80
Lys Gly Ala Cys Glu Ile Thr Arg Lys Thr Arg Arg Gln Cys Gln Ala
      85           90           95
Cys Arg Leu Arg Lys Cys Leu Glu Ser Gly Met Lys Lys Glu Met Ile
      100          105          110
Met Ser Asp Glu Ala Val Glu Glu Arg Arg Ala Leu Ile Lys Arg Lys
      115          120          125
Lys Ser Glu Arg Thr Gly Thr Gln Pro Leu Gly Val Gln Gly Leu Thr
      130          135          140
Glu Glu Gln Arg Met Met Ile Arg Glu Leu Met Asp Ala Gln Met Lys
      145          150          155          160
Thr Phe Asp Thr Thr Phe Ser His Phe Lys Asn Phe Arg Leu Pro Gly
      165          170          175
Val Leu Ser Ser Gly Cys Glu Leu Pro Glu Ser Leu Gln Ala Pro Ser
      180          185          190
Arg Glu Glu Ala Ala Lys Trp Ser Gln Val Arg Lys Asp Leu Cys Ser
      195          200          205
Leu Lys Val Ser Leu Gln Leu Arg Gly Glu Asp Gly Ser Val Trp Asn
      210          215          220
Tyr Lys Pro Pro Ala Asp Ser Gly Gly Lys Glu Ile Phe Ser Leu Leu
      225          230          235          240
Pro His Met Ala Asp Met Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser
      245          250          255
Phe Ala Lys Val Ile Ser Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln
      260          265          270
Ile Ser Leu Leu Lys Gly Ala Ala Phe Glu Leu Cys Gln Leu Arg Phe

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End
DI
Cont

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305					310					315					320
Glu	Pro	Met	Leu	Lys	Phe	His	Tyr	Met	Leu	Lys	Lys	Leu	Gln	Leu	His
				325					330					335	
Glu	Glu	Glu	Tyr	Val	Leu	Met	Gln	Ala	Ile	Ser	Leu	Phe	Ser	Pro	Asp
			340					345					350		
Arg	Pro	Gly	Val	Leu	Gln	His	Arg	Val	Val	Asp	Gln	Leu	Gln	Glu	Gln
		355					360					365			
Phe	Ala	Ile	Thr	Leu	Lys	Ser	Tyr	Ile	Glu	Cys	Asn	Arg	Pro	Gln	Pro
370					375						380				
Ala	His	Arg	Phe	Leu	Phe	Leu	Lys	Ile	Met	Ala	Met	Leu	Thr	Glu	Leu
385					390					395					400
Arg	Ser	Ile	Asn	Ala	Gln	His	Thr	Gln	Arg	Leu	Leu	Arg	Ile	Gln	Asp
			405					410						415	
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